

Fig. 1

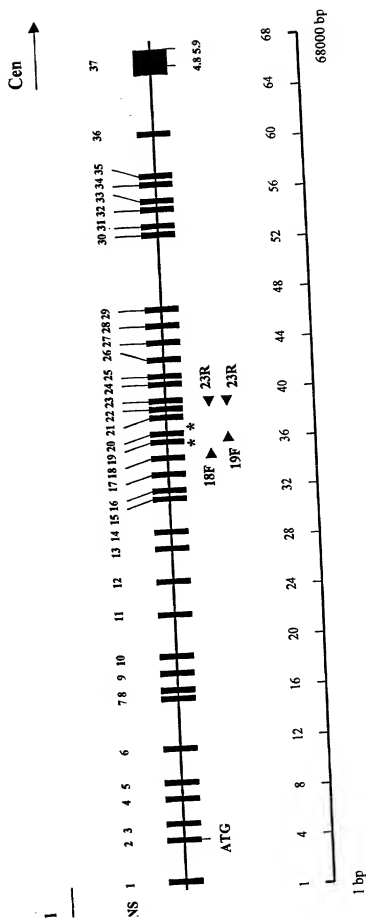


Fig. 2a

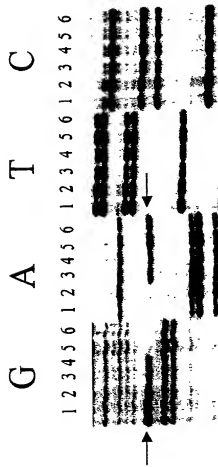


Fig. 2c

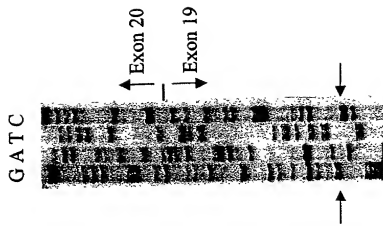


Fig. 2b

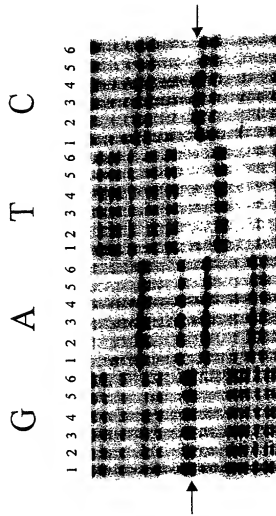


Fig. 3A

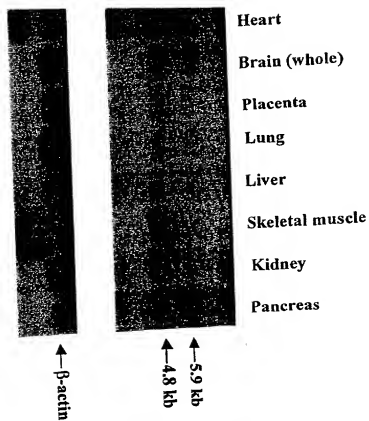
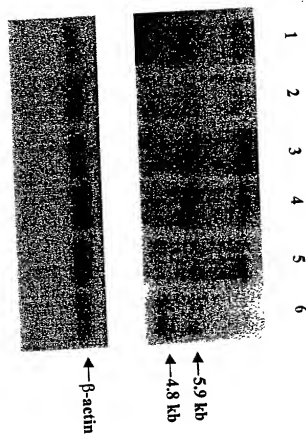


Fig. 3B

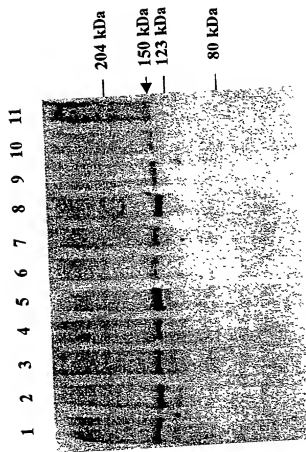


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FIG. 4A



FIG. 4B



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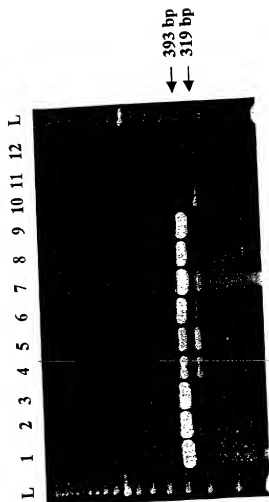


FIG. 5

FIGURE 6

IKBKAPgenomic.seq Length: 66479

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55751 AGAAAGGACC TGCAGTGGGA TCATAGAAAT TTTTGGCTTT GGATAGAAGC
55801 TATGTATGAT TCTGTCAATG GAGCTGGGAA TATACTTAC CACTTTTCA

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55851 AATTTCTTCT CTCTAGATGA AGTATACCAT ATTTTAAAGG TACTCTTCT
55901 CTTTGAGTTT GATGAACAAG GAAGGGAATT ACAGAAGGCC TTGAAAGATA
55951 CGCTGCAGTT GATGGAAAGG TCACTTCCAG AAATTTGGAC TCTTACTTAC
56001 CAGCAGAATT CAGCTACCCC GGTAAGTTT CTCAGAGACG GTGTGCATTT
56051 TTTTCATCAT TTTTCATGGT TATTGTATC ACACAATCTC CAAGTCAAAA
56101 AGTTTTCTTG TTCTTAAAC ATAAGATGCC ATAGTTAAAT TATCTAGCA
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56301 AATGAGTTG GAGTGGGGAG AGATGGGGGA AGATGGGGTC AGAGACGGCC
56351 TCTCACTTC CTTTCAGAAC TCAGGGATGG GATCAGGCTT TAAAGGGACC
56401 CCAGGCAATT GCTTTTCCTT TTGTTTTATG AAAAATTGA CTGTCACTT
56451 CTATGTTGT ATGATGGACT TTGCGGGTTG TGTTTAAAGC TGAATCAGT
56501 TTGATCGCA GAATTCTAGT ATATTGTCAT CTGTTTATTA TTTATACCTC
56551 TGTTCACTCT CTTACTTTC AAGTCTATTG TTAAGAGTTT TTATTTGGAT
56601 TCAAAAGGC TGGTGATCA GTCAAGATCT AGAAAGGAAA ACAAAGCCT
56651 ATCTATTATT TTATCACAGA ATTTAATATA TGGATTTGTT AAATAAGTAT
56701 TAGAGGACTA AACAAGGCAA AAGGGAAATA CAGAGGAAGC ACATTGAGAT
56751 AGTAACTGTA GGAAGCAGCT TTACCCTCTA GCTGAGGGAA CAGGAGGAGT
56801 TGTTGGGAAT TATTAGAATT TAGAAGCCTG GAAGTGGGGC CCTGTAGAC
56851 TGGCTCTTGA ACCTCTGAGA GGAGGGTGCC AGCCAGCTAA TCCTGGCATT
56901 TCTGAGGGAG CTGGTTCCAA GCGTACAGAA GTAAATGGAA ACTGGAAGGA
56951 ACAGCTGCTG CTGGGGGAAA AGCCAGCCGG TCGGGCCAGG TGTGGTGGTG
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57051 CTGAAGTCAG GAGTTCGTGA CTAATGTGGC CAACATGGAG AAGCCCCGTC
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57251 AGAGCGAATC TCCGTTTAAA AAAAAAAAAA AAAAAGCCAG CCAATCACGG
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57351 GGTGTTCACT GTAGGCAGGA CATGATGGGA AGCCAGCAGC AAGGAAGAAT
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58601 GGAGCACATG TGCACAGTTT CCATTCTGCT CCATAGTATG CACATGTTG

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58951 CAGGCTGTTT TCTGCTGGTA GGGATTGGC CTTTGGTATT GGCAGTCTTG
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59301 TAGCGGTGGG GGACCTGGTG CAGGAAAAATC CAGCATGACC ATTGTATGTG
59351 TAATTTTAA AAATATTTAT GTGGCATATG CTGTTCATA AAGGCACACC
59401 ACAGTTCAG TTTCAGTCTA AACTGTCTAC ATTTACATAT ACATCAAAAG
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60001 ACAGCTACCT TCCATCCAG CTAACCTCAT ACATCCAGAC TGTAACTACT

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61251 CACTGCAAGC TCCGCCTCCC GGGTTACGC CATTCTCTG CCTCACCTC
61301 CTGAGTAGCT GGGACTACAG GCGCCCGCCA TCACGCCCGG CTAATTTT
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FIGURE 7

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Figure 7
Continued

3181	cttcccagaa	tgcctaaact	tgataaaaaga	taaaaaacttg	tataacgaag	ctctgaagtt
3241	atattccacca	agctcacaaac	agtagaccaga	tatcagcatt	gcttattggg	agcacctgat
3301	gcaggagcaac	atgtatgagc	cagcggggct	catgtttgcc	cggtgcgggtg	ccacagagaa
3361	agctctctca	gcctttctca	catgtggcaa	ctggaagcaa	gocctctgtg	tggcagccca
3421	gcttaacttt	accaaagacc	agctgggtgg	cctcgccaga	actctggcag	gaaagctggt
3481	tgagcagagg	aagcacattg	atgcggccat	ggttttggaa	gagagtgcc	aggattatga
3541	agaagctgtg	ctcttgctgt	tagaaggagc	tgctgggaaa	gaagctttga	ggctggtata
3601	caaatataac	agactggata	ttatagaaac	caacgtaaa	ccttccattt	tagaagccca
3661	gaaaaattat	atggcatttc	tggactctca	gacagccaca	ttcagtgcgc	acaagaaacg
3721	tttattggta	gttcgagagc	tcaaggagca	agccagcag	cgaggctcgg	atgatgaggt
3781	accccacggg	caagagtcag	acctcttctc	tgaactagc	agtgtcgtga	gtggcagtg
3841	gatgagtgcc	aaatactccc	atagtaactc	caggatatca	cgcgatcat	ccaagaatcg
3901	ccgaaaagcg	gagcggaaga	agcacagcct	caaaagaagc	agtcgcgtcg	aggaacctg
3961	cctcctggag	gcactgagtg	aagtgtgtga	gaacactgaa	aacctgaaag	atgaagtata
4021	ccatatttta	aaggtactct	ttctctttga	gtttgatgaa	caaggaagg	aattacagaa
4081	ggcctttgaa	gatacgctgc	agttgatgga	aaggtcacct	ccagaaattt	ggactcttac
4141	ttaccagcag	aattcagcta	ccccggttct	aggtcccaat	tctactgcaa	atagatcat
4201	ggcatcttat	cagcaacaga	agacttcggt	tctctgtctt	gatctgcagc	tttttatacc
4261	accaaagatc	acacagaaga	cccagtgga	gctgagcctg	ctagactgag	tgcctgcagt
4321	taggagggat	ccgacagaga	agaccatttc	cactcaatcc	tgttgtctca	ccaccccttg
4381	ctctttgagg	gctggctatt	gagaactgga	aagagtaaaa	tgataactta	ccttagcatt
4441	gccaaagact	tcagcagaca	acaaagcaat	ctatttattt	tatgttgtgt	atgactcttg
4501	atcattagca	agacattaag	ctttaacctat	tatggcaaca	tttttgtgaa	atcattgttg
4561	tttcaactgg	gctgtttgag	agcataatta	tggtaatcat	gagattaatg	tttcatgatt
4621	tctacctcca	aagtgtgaag	acaagtaaaa	caatgttctt	aaattgtctt	attttgttgg
4681	cggaagaagt	tacaatggct	attagtgtca	catttggcca	aatgtaatca	ccttaaatgc
4741	ttcttgtcac	cttaaaactaa	agcagaataa	aaagtatcct	ttgaaattat	aagccctcct
4801	ttgctgacag	ctattatttt	gtaacatctt	accaggtcat	gtgctttcag	ttataactgg
4861	gctgagcctc	ctataattac	aatgtctata	gggactgttt	tactgctctg	gtatttttctg
4921	ctagagagtt	agcaatgta	gagctagaac	agattagaat	ttctaaacag	tatcatgcac
4981	agttgtgtgt	agtgtatcag	gtgcattgta	tggcatgcac	ggttgtgaat	tattctctgt
5041	ctccaaaata	ctgtttcttt	aactcaagata	tttttgtttg	tgtctaggcc	acttcattta
5101	tttttgtcta	tggtacttta	ctgacttctc	tttattcaat	tctccagccc	ctccacaaaa
5161	aaaactgtct	caaaaatgaga	atatttttat	tcttcatggt	gagcttagaa	aagcggccac
5221	ttcatctctga	ttaaaaaatt	cttccatggt	tttaaaatc	agaaccagac	cttcttact
5281	gtgtattcta	gccccattgt	gtctctataa	caacaacagc	ctttcaaagg	aactaataga
5341	gtgaaaactc	acctcattacc	acgaggaagt	acaaagcgat	tcacgtagga	tctgccccctg
5401	tgacaaaaac	acctccccatt	ggggccacct	tccaacacgt	gtgatcacat	ttcaaatatga
5461	ggtttaggga	aacaaatgcc	taaacctacg	cactgtacat	aaactaacag	gaaatgctgc
5521	ttttgtatct	caaaagaagt	atatagccaa	aattgttaatt	taagaagcct	ttgtcagtat
5581	agcaagatgt	taactataga	atcaactcag	gagtatccac	tgtaaaatct	aactttttctg
5641	tatgtttgaa	cattttcaca	atctcatagg	agtttttaaa	aagaagagaa	agaagatata
5701	ctttgctttg	gagaaatcta	ctttttgact	tacatgggtt	tgctgtaatt	agtgcccaaa
5761	tattgaaagg	gtcgaagtac	tttgttaatca	ctctttggca	tggtgtaata	agcatggtaa
5821	cttatattga	aatatagtcg	tcttgcgttg	gataactgta	aagggaacca	tgctgataga
5881	ctggaaatag	aagtaaatgt	gtttattgaa	aaaaaaaaa	aaaa	

10041556.016702

FIGURE 8

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1 mrnlklfrtl efrdiqpgpn pqcfslrteq gtvligsehg lievdpsvre vknevsivae
61 gflpedgsgr ivgvqdildq esvcvatasg dvlcslstq qlecvgsvas gisvmswspd
121 qelvilatgq qtlimtkdf epilegqihq ddfgeskfit vgwgrketqf hgsegrqaaf
181 qmqmhesalp wddhrpqvtw rgdqqffavs vvcpetgark vrvwnrefal qstsepvagl
241 gpalawkpsg sliastgdkp nqqdivffek ngllhghftl pflkdevkvn dllwnadssv
301 lavrledlqr ekssipktcv qlwtvgnyhw ylkqslsfst cgkskivslm wdpvtpyrh
361 vlcqgwhyla ydwhwttdrs vgdnsddlsn vavidgnrvl vtvfrqtvpv ppmctyqllf
421 phpvnqvftl ahpqksndla vldasnqisv ykcgdcpsad ptvklgavvg sgfkvclrt
481 hlekrykiqf ennedgdvnp lklglttwie edvflavshs efsprsvihh ltaasemde
541 ehgqlnvsss aavdgviisl ccnsktksvv lqladgqifk ylwespslai kpwknsqgfp
601 vrfpypctqt elamigeec vlgltdrcrf findievasn itsfavydef lllthshct
661 qcfcldrdsf ktlqaglsn hvshgevlrk vergsrivtv vpgdtklvlg mprgnlevvh
721 hralvlaqir kwldklmfke afecmrklri nlnpdydhnv kvflgnvetf ikqidsvnhi
781 nlfftelkee dvtktmypap vtssvylsrd pdgnkidlvc damravmesi nphkyclsil
841 tshvkkttpe leivlqkvhe lqgnapsdpd avsaeealky llhlvdvnel ydhslytydf
901 dlvlmvaeks qkdpkeylpf lntlkkmetn yqrftidkyl kryekaighl skcgppeyfe
961 cinlikdnl ynealklysp ssqqyqdisi aygehlmqeh nyepaglmfa rcgahekals
1021 afltcgnwkq alcvaaglnf tkdqlvglg tagklveqr khidaamvle esaqdyeeav
1081 llllegaawe ealrlvykyn rldlietnvk psileaqkny mafldsqtat fsrhkkrllv
1141 vrelkeqagq aglddevphg qesdlfsets svvgsemag kyshsnris arssknrrka
1201 erkkhslkeg spledlalle alsevvqnte nkdevyhil kvlflfeffe gqrelqkafe
1261 dtlqlmersl peiwtltyqq nsatpvlpgn stansimasy qqkqtsvpvl daelfippki
1321 nrrtqwkls1 ld

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10041856.010702

[illegible]

FIG. 1. Comparison of the amino acid sequence of Ikap across several species. Alignment of the amino acid sequence of Ikap (M_musculus) with that of *Homo sapiens* (H_sapiens), *Drosophila melanogaster* (D_melanogaster), *Saccharomyces cerevisiae* (S_cerevisiae), *Arabidopsis thaliana* (A_thaliana), and *Caenorhabditis elegans* (C_elegans). Black boxes indicate identical AA, while conserved AA residues are shown in gray. Asterisk (*) at AA position 696 for mouse and human proteins indicates the location of the heterozygous R696P mutation found in only 4 FD patients. Sequence alignments were made using Pileup and Boxshade commands from GCG Wisconsin Package V.9.0 (Madison, WI).

M_musculus 517 MSYSHS SCSMTHMLTVHSEVDEPQGLVSSSVTVGDGVVLGLCC SKTKS AVGLAD
H_sapiens 517 VSHSSTFPSPVHMLTASSESGEHCGLNVSSSVTVGDGVVLGLCC SKTKS AVGLAD
D_melanogaster 516 VHSSTFPSPVHMLTASSESGEHCGLNVSSSVTVGDGVVLGLCC SKTKS AVGLAD
S_cerevisiae 562 TQPLHMLTVHSEVDEPQGLVSSSVTVGDGVVLGLCC SKTKS AVGLAD
A_thaliana 486 HSHS SCSMTHMLTVHSEVDEPQGLVSSSVTVGDGVVLGLCC SKTKS AVGLAD
C_elegans 500 FVVDSPDSSESYTHVHSHKRLXS...RGANPEKIFPEENILGVNFSNRRHNASND

M_musculus 576 GULKILNWSPLSLAIPEKNSGCFVRFVHPTQEVANICGECVGLGLDTRCRFLVLT
H_sapiens 576 GCFVYVWSPLSLAIPEKNSGCFVRFVHPTQEVANICGECVGLGLDTRCRFLVLT
D_melanogaster 507 VGM...HEDADQIDNVIVK...EIVD...GVTGABGRLKRLHHLHGV
S_cerevisiae 604 GQNHETLKPGLVDRFVR...VHTSAEDDDNWSSESLVAFCHENLHHLHGV
A_thaliana 546 GQNHETLKPGLVDRFVR...VHTSAEDDDNWSSESLVAFCHENLHHLHGV
C_elegans 556 GQNHETLKPGLVDRFVR...VHTSAEDDDNWSSESLVAFCHENLHHLHGV

M_musculus 636 EVASNTISFA...VCDFFLLVTHSH...TCQCGSPSCASLRLGQAFSSSBA
H_sapiens 636 EVASNTISFA...VCDFFLLVTHSH...TCQCGSPSCASLRLGQAFSSSBA
D_melanogaster 548 EGHNTISFA...VCDFFLLVTHSH...TCQCGSPSCASLRLGQAFSSSBA
S_cerevisiae 659 LYSASVLSLE...VCDFFLLVTHSH...TCQCGSPSCASLRLGQAFSSSBA
A_thaliana 606 NLCCNCSSESYSELANEVTLSLELRQDFEFVTKKQDLVNGVGLGKFFVDCGRD
C_elegans 606 RVQCATSILTRG...SHTLDFDNEKFLDAG...

M_musculus 684 SGEH...RKRVVSGSRIVTVV...PDCRHLQMPGRGNLEVVHRAVLVAQIRKWLDRLEKE
H_sapiens 684 HGEV...RKRVVSGSRIVTVV...PDCRHLQMPGRGNLEVVHRAVLVAQIRKWLDRLEKE
D_melanogaster 584 S...RKRVVSGSRIVTVV...PDCRHLQMPGRGNLEVVHRAVLVAQIRKWLDRLEKE
S_cerevisiae 704 EDEB...VYARVGLVSGSRIVTVV...PDCRHLQMPGRGNLEVVHRAVLVAQIRKWLDRLEKE
A_thaliana 656 EDEB...VYARVGLVSGSRIVTVV...PDCRHLQMPGRGNLEVVHRAVLVAQIRKWLDRLEKE
C_elegans 638 GRTEDVNVVACEV...ACHSNG...VILCA...GNLLETQDRVVA...KTLQKRIA

M_musculus 741 AFECMRRLAINNLID...HNEKVELNVEFFV...PDSVNHILFFTELCEDEVKTKMYP
H_sapiens 741 AFECMRRLAINNLID...HNEKVELNVEFFV...PDSVNHILFFTELCEDEVKTKMYP
D_melanogaster 637 AHFMRKORINNLHIF...HNEKVELNVEFFV...PDSVNHILFFTELCEDEVKTKMYP
S_cerevisiae 761 AFVCRORINNLHIF...HNEKVELNVEFFV...PDSVNHILFFTELCEDEVKTKMYP
A_thaliana 726 AFVCRORINNLHIF...HNEKVELNVEFFV...PDSVNHILFFTELCEDEVKTKMYP
C_elegans 797 HNEKVELNVEFFV...PDSVNHILFFTELCEDEVKTKMYP

M_musculus 800 ...PITS...SVVSG...HFDCKRDLNCDAMRAAM...SAINPKFELS
H_sapiens 800 ...PITS...SVVSG...HFDCKRDLNCDAMRAAM...SAINPKFELS
D_melanogaster 696 ...PITS...SVVSG...HFDCKRDLNCDAMRAAM...SAINPKFELS
S_cerevisiae 820 ...PITS...SVVSG...HFDCKRDLNCDAMRAAM...SAINPKFELS
A_thaliana 786 ...PITS...SVVSG...HFDCKRDLNCDAMRAAM...SAINPKFELS
C_elegans 725 ...PITS...SVVSG...HFDCKRDLNCDAMRAAM...SAINPKFELS

M_musculus 839 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL
H_sapiens 839 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL
D_melanogaster 736 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL
S_cerevisiae 880 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL
A_thaliana 831 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL
C_elegans 797 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL

M_musculus 892 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL
H_sapiens 892 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL
D_melanogaster 782 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL
S_cerevisiae 926 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL
A_thaliana 891 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL
C_elegans 829 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL

M_musculus 951 ...SKCGPE...VFPECLNLIDR...NLYKEALGLYRPSQVQVQNS...GYVHLLKQEH
H_sapiens 951 ...SKCGPE...VFPECLNLIDR...NLYKEALGLYRPSQVQVQNS...GYVHLLKQEH
D_melanogaster 841 ...SKCGPE...VFPECLNLIDR...NLYKEALGLYRPSQVQVQNS...GYVHLLKQEH
S_cerevisiae 985 ...SKCGPE...VFPECLNLIDR...NLYKEALGLYRPSQVQVQNS...GYVHLLKQEH
A_thaliana 950 ...SKCGPE...VFPECLNLIDR...NLYKEALGLYRPSQVQVQNS...GYVHLLKQEH
C_elegans 889 ...SKCGPE...VFPECLNLIDR...NLYKEALGLYRPSQVQVQNS...GYVHLLKQEH

M_musculus 1002 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL
H_sapiens 1002 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL
D_melanogaster 892 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL
S_cerevisiae 1038 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL
A_thaliana 1095 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL
C_elegans 948 ...HVLQVKELOGNQ...PDP...SSVVEEALKYLLVLDVNNEL

Figure 9

Continued

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TABLE 2. COMPARISON OF THE NOVEL MOUSE *Ikbkap* GENE WITH MULTIPLE SPECIES HOMOLOGS

Species	Gene name	No. of amino acids	Molecular weight (kDa)	% aa identity with M.m.	GenBank Accession No.
<i>Mus musculus</i> (M.m.)	<i>Ikbkap</i>	1332	149.11	—	AF367244
<i>Homo sapiens</i>	<i>IKBKAP</i>	1332	149.11	80	AF153419
<i>Drosophila melanogaster</i>	<i>CG10535</i>	1213	138.21	32	AAF54670
<i>Saccharomyces cerevisiae</i>	<i>Elp1/Iki3p</i>	1349	152.99	29	AAB67278
<i>Arabidopsis thaliana</i>	Unknown	1308	146.63	27	BAB08695
<i>Caenorhabditis elegans</i>	Unknown	1177	134.80	24	AAF60430

Figure 10

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TABLE 1. MOUSE *Ikbk* EXON AND INTRON BOUNDARIES

Exon	Acceptor site	Donor site	Size (bp)	cDNA position
1		AGgtgagcattcgcgcg	129	1..129 ^a
2	tttttttccctcagAA	AAgttagctcactgagc	163	130..292 ^b
3	taatgcttgtagaagGT	AGgttaggttagaagcct	153	293..445
4	ttttctctgaicagCT	AGgttagcttgacagc*	82	446..527
5	acatgaactctaaGT	AGgttagcgtttctgg	81	528..608
6	cttgaacacitgagGC	TGgttaggcggagat	86	609..694
7	gtgtctctctcagCC	TGgtgtctctctcagc*	91	695..791
8	ctacctcctttcagAG	AAgttaggttagcataaa*	97	792..882
9	aggtctgctttcagAC	AGgttaggggtcagaagt	124	883..1006
10	ttttgctccacagGT	TGgttagcagctgtg	94	1007..1100
11	tccctccacacagTC	AAgttaggtgtctgcaa	231	1101..1331
12	cttttcattgtgtagAC	TGgttaggtggaagcagg	165	1332..1496
13	ttttgtttctagGT	TCgttaggtcttaata	100	1497..1596
14	ctaaatttgaacagGA	AGgttagctgttcatc	189	1597..1785
15	ttttttgcttttagTT	GGgttaggagtcagaagt	107	1786..1892
16	tttaatttacaacagAG	AGgttagaagacacggc	104	1893..1996
17	tttaattcttgcagGA	AGgttagtaggtctgtg	54	1997..2050
18	ttctgctgtgtagGT	AAgttagctctctata	106	2051..2156
19	cactggtatttttagTG	AGgttaggtgactcttc*	116	2157..2272
20	gggtttatttttagAT	AAgttagatttattct*	74	2273..2346
21	ttcgttctcacaagAC	AGgttagcctgtgctct	79	2347..2425
22	tactttctttagGT	AGgttagattttgata*	80	2426..2505
23	tactgtgtttctagGG	AAgttaggtgtgtgtgt	138	2506..2643
24	cacttacttccctagGT	AGgttaggacctgcgc*	86	2644..2729
25	cttaaacctccaagGA	AGgttaggtgagtttag*	149	2730..2878
26	aactttttcctagGA	TGgttaggggtttttt	124	2879..3002
27	ttttttttttcagGA	AGgttaggtgtgtgta*	98	3003..3100
28	cgtctcttctcagGC	AGgttagcaggccatt	202	3101..3302
29	tgtctgtctttcagGA	AGgttagcctctcccg	62	3303..3364
30	ctcttccctgtcagGA	TGgttaggaagcttga	63	3365..3427
31	ttttccctctttagGT	AGgttaggattacatt*	61	3428..3488
32	attatgctctcagCC	GGgttaggtctccaaa*	114	3489..3602
33	gttcatctcttagAT	GCgttagctcagagact*	112	3603..3714
34	tgtaatcttgcagGA	AGgttaggtctcaggtc	128	3715..3842
35	ccatttctcttagAT	CGgttagctctcaga	155	3843..3997
36	ctgtttctgtagGT	CGgttagctgtctgtc	76	3998..4073
37	catctgtctcagAT		709	4074..4799 ^c

Figure 11

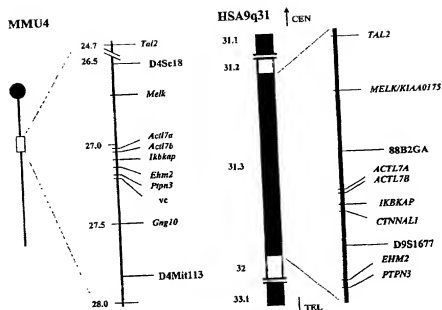


Figure 12